

WHAT IS CLAIMED IS:

1. A bacterial effector protein which inhibits programmed cell death in eukaryotes.
- 5 2. The bacterial effector protein according to claim 1, wherein the protein has an amino acid sequence of SEQ. ID. NOS: 2, 4, 6, or 8.
3. The bacterial effector protein according to claim 1, wherein the protein has an amino acid motif selected from the group consisting of the
10 motif of SEQ ID NO:9, the motif of SEQ ID NO:10, the motif of SEQ ID NO:11, the motif of SEQ ID NO:12, the motif of SEQ ID NO:13, the motif of SEQ ID NO:14, the motif of SEQ ID NO:15, the motif of SEQ ID NO:16, the motif of SEQ ID NO:17, the motif of SEQ ID NO:18, the motif of SEQ ID NO:19, the motif of SEQ ID NO:20, the motif of SEQ ID NO:21, the motif of SEQ ID
15 NO:22, the motif of SEQ ID NO:23, and combinations thereof.
4. The bacterial effector protein according to claim 1, wherein the protein has an amino acid sequence of SEQ ID NO:24.
- 20 5. The bacterial effector protein according to claim 1, wherein the protein has an amino acid sequence spanning a C-terminus of SEQ. ID. NOS: 2, 4, 6, or 8.
6. The bacterial effector protein according to claim 1, wherein
25 the protein has an amino acid sequence spanning amino acids 308 and 553 of SEQ. ID. NO: 2.
7. A nucleic acid molecule encoding a protein according to claim 1.
- 30 8. The nucleic acid molecule according to claim 7, wherein the protein has an amino acid sequence of SEQ. ID. NOS: 2, 4, 6, or 8.

9. The nucleic acid molecule according to claim 7, wherein the protein has an amino acid motif selected from the group consisting of the motif of SEQ ID NO:9, the motif of SEQ ID NO:10, the motif of SEQ ID NO:11, the motif of SEQ ID NO:12, the motif of SEQ ID NO:13, the motif of SEQ ID NO:14, the motif of SEQ ID NO:15, the motif of SEQ ID NO:16, the motif of SEQ ID NO:17, the motif of SEQ ID NO:18, the motif of SEQ ID NO:19, the motif of SEQ ID NO:20, the motif of SEQ ID NO:21, the motif of SEQ ID NO:22, the motif of SEQ ID NO:23, and combinations thereof.

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10. The nucleic acid molecule according to claim 7, wherein the protein has an amino acid sequence of SEQ ID NO:24.

11. The nucleic acid molecule according to claim 7, wherein the protein has an amino acid sequence spanning a C-terminus of SEQ. ID. NOS: 2, 4, 6, or 8.

12. The nucleic acid molecule according to claim 7, wherein the protein has an amino acid sequence spanning amino acids 308 and 553 of SEQ. ID. NO: 2.

13. The nucleic acid molecule according to claim 7, wherein the nucleic acid molecule either: (1) has a nucleotide sequence of SEQ. ID. NOS: 1, 3, 5, or 7; (2) has a nucleotide sequence that is at least 85% similar to the nucleotide sequence of SEQ. ID. NOS: 1, 3, 5, or 7 by basic BLAST using default parameters analysis; or (3) hybridizes to the nucleotide sequence of SEQ. ID. NOS: 1, 3, 5, or 7 under stringency conditions characterized by a hybridization buffer comprising 5X SSC buffer at a temperature of 54°C.

14. An expression vector containing the nucleic acid molecule according to claim 7.

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15. A host cell transformed with the nucleic acid molecule according to claim 7.
16. The host cell according to claim 15, wherein the host cell is
5 a eukaryote.
17. The host cell according to claim 16, wherein the host cell is a plant cell.
18. The host cell according to claim 16, wherein the host cell is
10 a yeast cell.
19. The host cell according to claim 16, wherein the host cell is a mammalian or an invertebrate cell.
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20. A transgenic plant transformed with the nucleic acid molecule according to claim 7.
21. The transgenic plant according to claim 20, wherein the
20 protein has an amino acid sequence of SEQ. ID. NOS: 2, 4, 6, or 8.
22. The transgenic plant according to claim 20, wherein the protein has an amino acid motif selected from the group consisting of the motif of
25 SEQ ID NO:9, the motif of SEQ ID NO:10, the motif of SEQ ID NO:11, the motif of SEQ ID NO:12, the motif of SEQ ID NO:13, the motif of SEQ ID NO:14, the motif of SEQ ID NO:15, the motif of SEQ ID NO:16, the motif of SEQ ID NO:17, the motif of SEQ ID NO:18, the motif of SEQ ID NO:19, the motif of SEQ ID NO:20, the motif of SEQ ID NO:21, the motif of SEQ ID NO:22, the motif of SEQ ID NO:23, and combinations thereof.
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23. The transgenic plant according to claim 20, wherein the protein has an amino acid sequence of SEQ ID NO:24.

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24. The transgenic plant according to claim 20, wherein the protein has an amino acid sequence spanning a C-terminus of SEQ. ID. NOS: 2, 4, 6, or 8.

5 25. The transgenic plant according to claim 20, wherein the protein has an amino acid sequence spanning amino acids 308 and 553 of SEQ. ID. NO: 2.

10 26. The transgenic plant according to claim 20, wherein the plant is selected from the group consisting of rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper, celery carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, strawberry, grape, raspberry, pineapple, soybean, tobacco tomato, sorghum,
15 sugarcane, and banana.

27. The transgenic plant according to claim 20, wherein the plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, roses, and zinnia.
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28. A transgenic plant seed transformed with the nucleic acid molecule according to claim 7.

29. The transgenic plant seed according to claim 28, wherein
25 the protein has an amino acid sequence of SEQ. ID. NOS: 2, 4, 6, or 8.

30. The transgenic plant seed according to claim 28, wherein the protein has an amino acid motif selected from the group consisting of the motif of SEQ ID NO:9, the motif of SEQ ID NO:10, the motif of SEQ ID NO:11,
30 the motif of SEQ ID NO:12, the motif of SEQ ID NO:13, the motif of SEQ ID NO:14, the motif of SEQ ID NO:15, the motif of SEQ ID NO:16, the motif of SEQ ID NO:17, the motif of SEQ ID NO:18, the motif of SEQ ID NO:19, the

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motif of SEQ ID NO:20, the motif of SEQ ID NO:21, the motif of SEQ ID NO:22, the motif of SEQ ID NO:23, and combinations thereof.

31. The transgenic plant seed according to claim 28, wherein
5 the protein has an amino acid sequence of SEQ ID NO:24.

32. The transgenic plant seed according to claim 28, wherein
the protein has an amino acid sequence spanning a C-terminus of SEQ. ID. NOS:
2, 4, 6, or 8.

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33. The transgenic plant seed according to claim 28, wherein
the protein has an amino acid sequence spanning amino acids 308 and 553 of
SEQ. ID. NO: 2.

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34. The transgenic plant seed according to claim 28, wherein
the plant is selected from the group consisting of rice, wheat, barley, rye, cotton,
sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive,
cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant,
pepper, celery carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon,
20 strawberry, grape, raspberry, pineapple, soybean, tobacco tomato, sorghum,
sugarcane, and banana.

35. The transgenic plant seed according to claim 28, wherein
the plant is selected from the group consisting of *Arabidopsis thaliana*,
25 *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, roses,
and zinnia.

36. A method of suppressing programmed cell death in
eukaryotes comprising:
30 transforming a eukaryote with a nucleic acid according to claim 7
and
growing the eukaryote under conditions effective to suppress
programmed cell death in the eukaryote.

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37. The method according to claim 36, wherein the protein has an amino acid sequence of SEQ. ID. NOS: 2, 4, 6, or 8.

5 38. The method according to claim 36, wherein the protein has an amino acid motif selected from the group consisting of the motif of SEQ ID NO:9, the motif of SEQ ID NO:10, the motif of SEQ ID NO:11, the motif of SEQ ID NO:12, the motif of SEQ ID NO:13, the motif of SEQ ID NO:14, the motif of SEQ ID NO:15, the motif of SEQ ID NO:16, the motif of SEQ ID NO:17, the
10 motif of SEQ ID NO:18, the motif of SEQ ID NO:19, the motif of SEQ ID NO:20, the motif of SEQ ID NO:21, the motif of SEQ ID NO:22, the motif of SEQ ID NO:23, and combinations thereof.

39. The method according to claim 36, wherein the protein has
15 an amino acid sequence of SEQ ID NO:24.

40. The method according to claim 36, wherein the protein has an amino acid sequence spanning a C-terminus of SEQ. ID. NOS: 2, 4, 6, or 8.

20 41. The method according to claim 36, wherein the protein has an amino acid sequence spanning amino acids 308 and 553 of SEQ. ID. NO: 2.

42. The method according to claim 36, wherein the eukaryote is yeast.
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43. The method according to claim 36, wherein the eukaryote is a mammal or an invertebrate.

44. The method according to claim 36, wherein the eukaryote is
30 a plant.

45. The method according to claim 44, wherein the plant is selected from the group consisting of rice, wheat, barley, rye, cotton, sunflower,

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peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage,
cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper,
celery carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon,
strawberry, grape, raspberry, pineapple, soybean, tobacco tomato, sorghum,
5 sugarcane, and banana.

46. The method according to claim 44, wherein the plant is
selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia,
pelargonium, poinsettia, chrysanthemum, carnation, roses, and zinnia.

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47. A method of delaying senescence in plants comprising:
transforming a plant with a nucleic acid according to claim 7 and
growing the plant under conditions effective to delay senescence in
the plant.

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48. The method according to claim 47, wherein the protein has
an amino acid sequence of SEQ. ID. NOS: 2, 4, 6, or 8.

49. The method according to claim 47, wherein the protein has
20 an amino acid motif selected from the group consisting of the motif of SEQ ID
NO:9, the motif of SEQ ID NO:10, the motif of SEQ ID NO:11, the motif of SEQ
ID NO:12, the motif of SEQ ID NO:13, the motif of SEQ ID NO:14, the motif of
SEQ ID NO:15, the motif of SEQ ID NO:16, the motif of SEQ ID NO:17, the
motif of SEQ ID NO:18, the motif of SEQ ID NO:19, the motif of SEQ ID
25 NO:20, the motif of SEQ ID NO:21, the motif of SEQ ID NO:22, the motif of
SEQ ID NO:23, and combinations thereof.

50. The method according to claim 47, wherein the protein has
an amino acid sequence of SEQ ID NO:24.

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51. The method according to claim 47, wherein the protein has
an amino acid sequence spanning a C-terminus of SEQ. ID. NOS: 2, 4, 6, or 8.

52. The method according to claim 47, wherein the protein has an amino acid sequence spanning amino acids 308 and 553 of SEQ. ID. NO: 2.

53. The method according to claim 47, wherein the plant is
5 selected from the group consisting of rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper, celery carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, strawberry, grape, raspberry, pineapple, soybean, tobacco tomato, sorghum,
10 sugarcane, and banana.

54. The method according to claim 47, wherein the plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, roses, and zinnia.

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55. A method of increasing protein expression in plants comprising:

transforming a plant with a nucleic acid encoding a first protein according to claim 1 and a second protein which is toxic to plants and

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growing the plant under conditions effective to increase expression of the second protein in the plant.

56. The method according to claim 55, wherein the first protein has an amino acid sequence of SEQ. ID. NOS: 2, 4, 6, or 8.

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57. The method according to claim 55, wherein the first protein has an amino acid motif selected from the group consisting of the motif of SEQ ID NO:9, the motif of SEQ ID NO:10, the motif of SEQ ID NO:11, the motif of SEQ ID NO:12, the motif of SEQ ID NO:13, the motif of SEQ ID NO:14, the
30 motif of SEQ ID NO:15, the motif of SEQ ID NO:16, the motif of SEQ ID NO:17, the motif of SEQ ID NO:18, the motif of SEQ ID NO:19, the motif of SEQ ID NO:20, the motif of SEQ ID NO:21, the motif of SEQ ID NO:22, the motif of SEQ ID NO:23, and combinations thereof.

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58. The method according to claim 55, wherein the protein has an amino acid sequence of SEQ ID NO:24.

5 59. The method according to claim 55, wherein the first protein has an amino acid sequence spanning a C-terminus of SEQ. ID. NOS: 2, 4, 6, or 8.

60. The method according to claim 55, wherein the first protein has an amino acid sequence spanning amino acids 308 and 553 of SEQ. ID. NO:2.

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61. The method according to claim 55, wherein the plant is selected from the group consisting of rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper,
15 celery carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, strawberry, grape, raspberry, pineapple, soybean, tobacco tomato, sorghum, sugarcane, and banana.

62. The method according to claim 55, wherein the plant is
20 selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, roses, and zinnia.

63. A nucleic acid construct comprising:
a nucleic acid molecule encoding a first protein according
25 to claim 1 and coupled to a nucleic acid molecule producing a second protein toxic to eukaryotes.

64. The nucleic acid construct according to claim 63, wherein the first protein has an amino acid sequence of SEQ. ID. NOS: 2, 4, 6, or 8.

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65. The nucleic acid construct according to claim 63, wherein the first protein has an amino acid motif selected from the group consisting of the motif of SEQ ID NO:9, the motif of SEQ ID NO:10, the motif of SEQ ID NO:11,

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the motif of SEQ ID NO:12, the motif of SEQ ID NO:13, the motif of SEQ ID NO:14, the motif of SEQ ID NO:15, the motif of SEQ ID NO:16, the motif of SEQ ID NO:17, the motif of SEQ ID NO:18, the motif of SEQ ID NO:19, the motif of SEQ ID NO:20, the motif of SEQ ID NO:21, the motif of SEQ ID NO:22, the motif of SEQ ID NO:23, and combinations thereof.

66. The nucleic acid construct according to claim 63, wherein the protein has an amino acid sequence of SEQ ID NO:24.

10 67. The nucleic acid construct according to claim 63, wherein the first protein has an amino acid sequence spanning a C-terminus of SEQ. ID. NOS: 2, 4, 6, or 8.

15 68. The nucleic acid construct according to claim 63, wherein the first protein has an amino acid sequence spanning amino acids 308 and 553 of SEQ. ID. NO: 2.

69. The nucleic acid construct according to claim 63, wherein the eukaryote is yeast.

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70. The nucleic acid construct according to claim 63, wherein the eukaryote is a mammal or an invertebrate.

71. The nucleic acid construct according to claim 63, wherein the eukaryote is a plant.

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72. An expression vector containing the nucleic acid construct according to claim 63.

30 73. A host cell transduced with the nucleic acid construct according to claim 63.

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74. The host cell according to claim 73, wherein the host cell is a eukaryote.
75. The host cell according to claim 74, wherein the eukaryote is yeast.
76. The host cell according to claim 74, wherein the eukaryote is a mammal or invertebrate.
77. The host cell according to claim 74, wherein the eukaryote is a plant.
78. A transgenic plant transformed with the nucleic acid construct according to claim 63.
79. The transgenic plant according to claim 78, wherein the first protein has an amino acid sequence of SEQ. ID. NOS: 2, 4, 6, or 8.
80. The transgenic plant according to claim 78, wherein the first protein has an amino acid motif selected from the group consisting of the motif of SEQ ID NO:9, the motif of SEQ ID NO:10, the motif of SEQ ID NO:11, the motif of SEQ ID NO:12, the motif of SEQ ID NO:13, the motif of SEQ ID NO:14, the motif of SEQ ID NO:15, the motif of SEQ ID NO:16, the motif of SEQ ID NO:17, the motif of SEQ ID NO:18, the motif of SEQ ID NO:19, the motif of SEQ ID NO:20, the motif of SEQ ID NO:21, the motif of SEQ ID NO:22, the motif of SEQ ID NO:23, and combinations thereof.
81. The transgenic plant according to claim 78, wherein the protein has an amino acid sequence of SEQ ID NO:24.
82. The transgenic plant according to claim 78, wherein the first protein has an amino acid sequence spanning a C-terminus of SEQ. ID. NOS: 2, 4, 6, or 8.

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83. The transgenic plant according to claim 78, wherein the first protein has an amino acid sequence spanning amino acids 308 and 553 of SEQ. ID. NO: 2.

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84. The transgenic plant according to claim 78, wherein the plant is selected from the group consisting of rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper, celery carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, strawberry, grape, raspberry, pineapple, soybean, tobacco tomato, sorghum, sugarcane, and banana.

85. The transgenic plant according to claim 78, wherein the plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, roses, and zinnia.

86. A transgenic plant seed transduced with the nucleic acid construct according to claim 63.

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87. The transgenic plant seed according to claim 86, wherein the first protein has an amino acid sequence of SEQ. ID. NOS: 2, 4, 6, or 8.

88. The transgenic plant seed according to claim 86, wherein the first protein has an amino acid motif selected from the group consisting of the motif of SEQ ID NO:9, the motif of SEQ ID NO:10, the motif of SEQ ID NO:11, the motif of SEQ ID NO:12, the motif of SEQ ID NO:13, the motif of SEQ ID NO:14, the motif of SEQ ID NO:15, the motif of SEQ ID NO:16, the motif of SEQ ID NO:17, the motif of SEQ ID NO:18, the motif of SEQ ID NO:19, the motif of SEQ ID NO:20, the motif of SEQ ID NO:21, the motif of SEQ ID NO:22, the motif of SEQ ID NO:23, and combinations thereof.

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89. The transgenic plant seed according to claim 86, wherein the protein has an amino acid sequence of SEQ ID NO:24.

90. The transgenic plant seed according to claim 86, wherein
5 the first protein has an amino acid sequence spanning a C-terminus of SEQ. ID. NOS: 2, 4, 6, or 8.

91. The transgenic plant seed according to claim 86, wherein the first protein has an amino acid sequence spanning amino acids 308 and 553 of
10 SEQ. ID. NO: 2.

92. The transgenic plant seed according to claim 86, wherein the plant is selected from the group consisting of rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive,
15 cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper, celery carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, strawberry, grape, raspberry, pineapple, soybean, tobacco tomato, sorghum, sugarcane, and banana.

93. The transgenic plant seed according to claim 86, wherein the plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, roses, and zinnia.

94. A method of stabilizing a transgenic plant producing a protein toxic to plants comprising:
providing a transgenic plant transduced with a nucleic acid molecule encoding a first protein according to claim 1 and a nucleic acid molecule producing a protein toxic to plants and
25 growing the plant under conditions effective to stabilize the plant.
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95. The method according to claim 94, wherein the nucleic acid molecule encoding the first protein and the nucleic acid molecule producing a protein toxic to plants are coupled together.

5 96. The method according to claim 94, wherein the first protein has an amino acid sequence of SEQ. ID. NOS: 2, 4, 6, or 8.

97. The method according to claim 94, wherein the first protein has an amino acid motif selected from the group consisting of the motif of SEQ
10 ID NO:9, the motif of SEQ ID NO:10, the motif of SEQ ID NO:11, the motif of SEQ ID NO:12, the motif of SEQ ID NO:13, the motif of SEQ ID NO:14, the motif of SEQ ID NO:15, the motif of SEQ ID NO:16, the motif of SEQ ID NO:17, the motif of SEQ ID NO:18, the motif of SEQ ID NO:19, the motif of SEQ ID NO:20, the motif of SEQ ID NO:21, the motif of SEQ ID NO:22, the
15 motif of SEQ ID NO:23, and combinations thereof.

98. The method according to claim 94, wherein the protein has an amino acid sequence of SEQ ID NO:24.

20 99. The method according to claim 94, wherein the first protein has an amino acid sequence spanning a C-terminus of SEQ. ID. NOS: 2, 4, 6, or 8.

100. The method according to claim 94, wherein the first protein has an amino acid sequence spanning amino acids 308 and 553 of SEQ. ID. NO:2.

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101. The method according to claim 94, wherein the plant is selected from the group consisting of rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper,
30 celery carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, strawberry, grape, raspberry, pineapple, soybean, tobacco tomato, sorghum, sugarcane, and banana.

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102. The method according to claim 94, wherein the plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, roses, and zinnia.

5 103. A method of treating a subject for a condition mediated by programmed cell death comprising:

 administering to the subject a protein according to claim 1 under conditions effective to treat the condition mediated by programmed cell death.

10 104. The method according to claim 103, wherein the protein has an amino acid sequence of SEQ. ID. NOS: 2, 4, 6, or 8.

 105. The method according to claim 103, wherein the first protein has an amino acid motif selected from the group consisting of the motif of
15 SEQ ID NO:9, the motif of SEQ ID NO:10, the motif of SEQ ID NO:11, the motif of SEQ ID NO:12, the motif of SEQ ID NO:13, the motif of SEQ ID NO:14, the motif of SEQ ID NO:15, the motif of SEQ ID NO:16, the motif of SEQ ID NO:17, the motif of SEQ ID NO:18, the motif of SEQ ID NO:19, the motif of SEQ ID NO:20, the motif of SEQ ID NO:21, the motif of SEQ ID NO:22, the
20 motif of SEQ ID NO:23, and combinations thereof.

 106. The method according to claim 103, wherein the protein has an amino acid sequence of SEQ ID NO:24.

25 107. The method according to claim 103, wherein the protein has an amino acid sequence spanning a C-terminus of SEQ. ID. NOS: 2, 4, 6, or 8.

 108. The method according to claim 103, wherein the protein has an amino acid sequence spanning amino acids 308 and 553 of SEQ. ID. NO: 2.

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 109. The method according to claim 103, wherein the condition is selected from the group consisting of Parkinson's disease, Alzheimer's disease, hepatitis, acute liver injury, hepatitis, and inflammation.